



results of BLAST

BLASTN 2.2.12 [Aug-07-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1126736645-6349-116079271193.BLASTQ1

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
3,491,285 sequences; 15,298,534,039 total letters

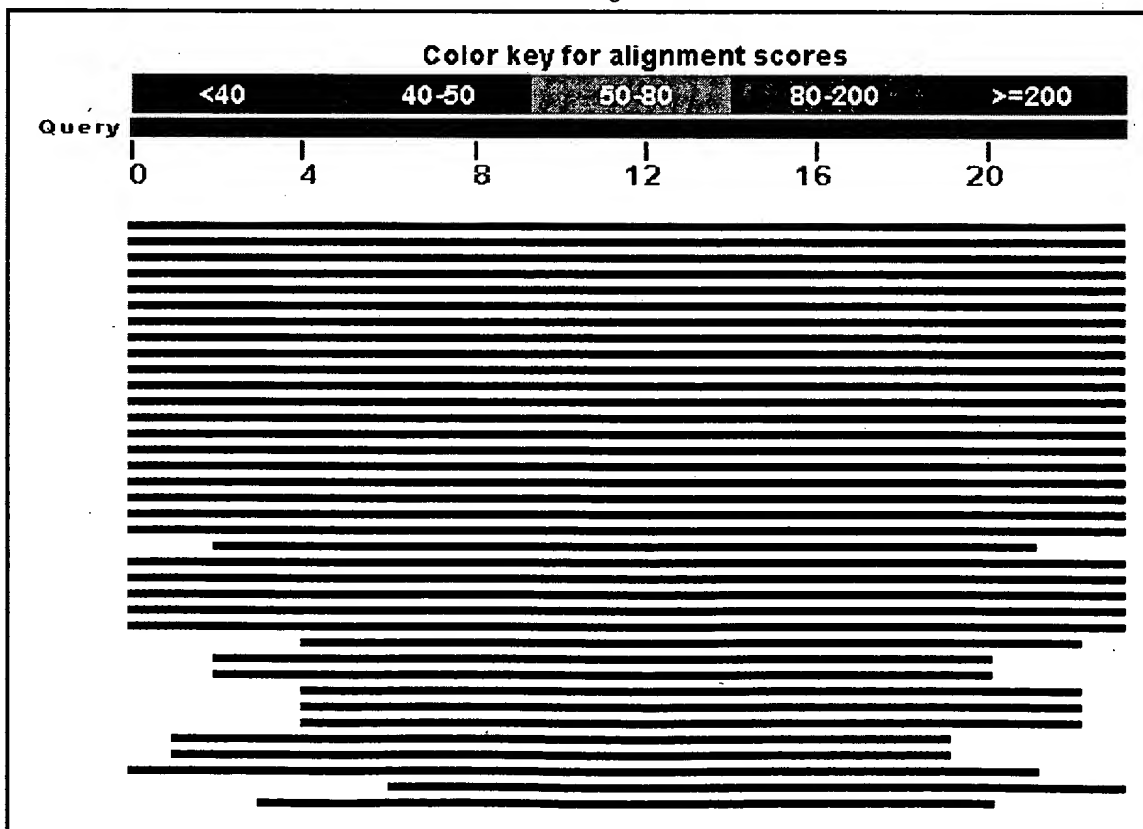
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=

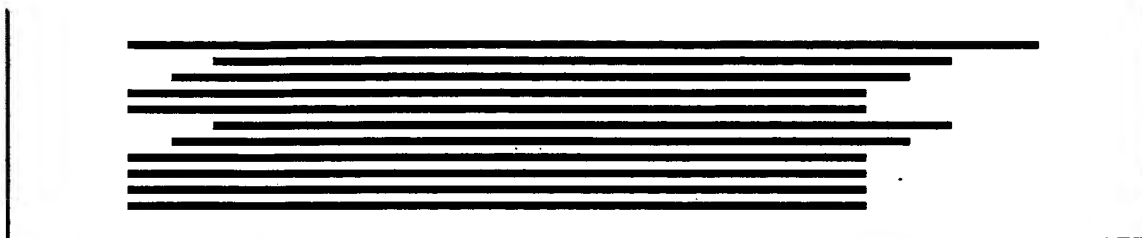
(23 letters)

Distribution of 48 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



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Sequences producing significant alignments:			Score (Bits)	E Value	
gi 55645360 ref XM_511474.1 	PREDICTED: Pan troglodytes DNA t...		46.1	0.001	G
gi 19913405 ref NM_001067.2 	Homo sapiens topoisomerase (DNA) II		46.1	0.001	U
gi 15488575 gb BC013429.1 	Homo sapiens topoisomerase (DNA) I...		46.1	0.001	U
gi 292829 gb J04088.1 HUMTOPII	Human DNA topoisomerase II (top2)		46.1	0.001	U
gi 19913407 ref NM_001068.2 	Homo sapiens topoisomerase (DNA) II		38.2	0.25	U
gi 73990501 ref XM_534241.2 	PREDICTED: Canis familiaris simi...		38.2	0.25	G
gi 73966010 ref XM_857989.1 	PREDICTED: Canis familiaris simi...		38.2	0.25	G
gi 73966008 ref XM_537646.2 	PREDICTED: Canis familiaris simi...		38.2	0.25	G
gi 55619958 ref XM_516332.1 	PREDICTED: Pan troglodytes DNA t...		38.2	0.25	G
gi 45382160 ref NM_204791.1 	Gallus gallus topoisomerase (DNA) I		38.2	0.25	U
gi 587514 emb Z46372.1 RNDNATI2	R.norvegicus RNA for DNA topoiso		38.2	0.25	E
gi 57963 emb Z19552.1 RNDNATPII	R.norvegicus mRNA for DNA topoiso		38.2	0.25	U
gi 2909392 emb Y16595.1 CLTOPO4	Cricetulus longicaudatus mRNA...		38.2	0.25	
gi 2909390 emb Y16594.1 CLTOPO3	Cricetulus longicaudatus mRNA...		38.2	0.25	
gi 37230 emb X68060.1 HSTOPIIB	H.sapiens topIIB mRNA for topoiso		38.2	0.25	U
gi 55725809 emb CR857392.1 	Pongo pygmaeus mRNA; cDNA DKFZp46...		38.2	0.25	
gi 62087337 dbj AB208879.1 	Homo sapiens mRNA for DNA topoiso...		38.2	0.25	G
gi 38259191 ref NM_022183.2 	Rattus norvegicus topoisomerase (DN		38.2	0.25	U
gi 6755848 ref NM_011623.1 	Mus musculus topoisomerase (DNA) II		38.2	0.25	U
gi 10121856 gb AF285155.1 AF285155	Gallus gallus topoisomeras...		38.2	0.25	U
gi 27452890 gb AC137053.2 	Homo sapiens 12 BAC RP11-64103 (Ro...		38.2	0.25	
gi 54400871 gb AC122444.4 	Mus musculus BAC clone RP24-23219 fro		38.2	0.25	
gi 6714552 dbj AB007445.2 	Gallus gallus mRNA for DNA topoisomer		38.2	0.25	U
gi 220615 dbj D12513.1 MUSTOP2	Mouse mRNA for DNA topoisomerase		38.2	0.25	U
gi 339809 gb M27504.1 HUMTOPIIX	Homo sapiens topoisomerase type		38.2	0.25	U
gi 191217 gb L04607.1 CRUTOPISII	Cricetulus griseus DNA topoisom		38.2	0.25	
gi 50911806 ref XM_467311.1 	Oryza sativa (japonica cultivar-gro		36.2	0.98	G
gi 33457259 gb AC125538.4 	Mus musculus BAC clone RP24-178B2 ...		36.2	0.98	
gi 19909460 gb AC098708.3 	Mus musculus BAC clone RP23-1116 from		36.2	0.98	
gi 58530788 dbj AP008208.1 	Oryza sativa (japonica cultivar-g...		36.2	0.98	
gi 41052945 dbj AP004778.3 	Oryza sativa (japonica cultivar-g...		36.2	0.98	
gi 32982494 dbj AK072471.1 	Oryza sativa (japonica cultivar-g...		36.2	0.98	U
gi 57226287 gb AE017344.1 	Cryptococcus neoformans var. neofo...		36.2	0.98	
gi 58266227 ref XM_570270.1 	Filobasidiella neoformans expres...		36.2	0.98	G
gi 32399348 emb BX546470.1 	Human DNA sequence from clone WI2...		34.2	3.9	
gi 15591148 emb AL391425.25 	Human DNA sequence from clone RP...		34.2	3.9	
gi 22531393 emb AL359918.43 	Human DNA sequence from clone RP...		34.2	3.9	
gi 7800095 emb AL118517.17 HSJ125M10	Human DNA sequence from ...		34.2	3.9	
gi 6997161 gb AC023838.1 	Arabidopsis thaliana chromosome III...		34.2	3.9	

gi 15920116 gb AC093744.2 	Homo sapiens BAC clone RP11-25B14 fro	34.2	3.9
gi 3132359 dbj AP000049.1 	Homo sapiens genomic DNA, chromoso...	34.2	3.9
gi 37537450 dbj BS000183.1 	Pan troglodytes chromosome 22 clo...	34.2	3.9
gi 5672531 dbj AP000385.1 	Arabidopsis thaliana genomic DNA, chr	34.2	3.9
gi 15883118 emb AJ338700.1 	HSA338700 Homo sapiens genomic seq...	34.2	3.9
gi 7768718 dbj AP001718.1 	Homo sapiens genomic DNA, chromosome	34.2	3.9
gi 4826584 dbj AP000193.1 	Homo sapiens genomic DNA, chromoso...	34.2	3.9
gi 4835680 dbj AP000311.1 	Homo sapiens genomic DNA, chromoso...	34.2	3.9
gi 4730851 dbj AP000117.1 	Homo sapiens genomic DNA of 21q22....	34.2	3.9

E

Alignments

Get selected sequences

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Deselect all

> [gi|55645360|ref|XM_511474.1|](#) **U E G** PREDICTED: Pan troglodytes DNA topoisomerase II, (LOC454651), mRNA
Length=3081

Score = 46.1 bits (23), Expect = 0.001
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Minus

Query 1 ATTTTCCATGATCTGCTTATGAG 23
|||||
Sbjct 1380 ATTTTCCATGATCTGCTTATGAG 1358

> [gi|19913405|ref|NM_001067.2|](#) **U E G** Homo sapiens topoisomerase (DNA) II alpha 170kDa, clone IMAGE:4101949
Length=5698

Score = 46.1 bits (23), Expect = 0.001
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Minus

Query 1 ATTTTCCATGATCTGCTTATGAG 23
|||||
Sbjct 1638 ATTTTCCATGATCTGCTTATGAG 1616

> [gi|15488575|gb|BC013429.1|](#) **U E G** Homo sapiens topoisomerase (DNA) II alpha 170kDa, clone IMAGE:4101949
Length=3076

Score = 46.1 bits (23), Expect = 0.001
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Minus

Query 1 ATTTTCCATGATCTGCTTATGAG 23
|||||
Sbjct 1638 ATTTTCCATGATCTGCTTATGAG 1616

> [gi|292829|gb|J04088.1|HUMTOPII](#) **U E G** Human DNA topoisomerase II (top2) mRNA, complete cds
Length=4792

Score = 46.1 bits (23), Expect = 0.001